



SEQUENCE LISTING

<110> H. Robert
Hengartner, Michael

<120> IDENTIFICATION AND CHARACTERIZATION OF A
GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
USES THEREOF

<130> 01997/201006

<140> US 09/993,420

<141> 2001-11-06

<150> 09/234,186

<151> 1999-01-20

<150> 07/898,933

<151> 1992-06-12

<150> 07/927,681

<151> 1992-08-10

<150> 08/288,295

<151> 1994-08-10

<150> 08/801,248

<151> 1997-02-19

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 6560

<212> DNA

<213> Caenorhabditis elegans

<220>

<221> misc_feature

<222> (1)...(6559)

<223> n = A,T,C or G

<400> 1

atcgatagtc	gtcaccaaat	ggattttccg	atttctcact	agtccatggc	tcacaattta	60
caaaatctcg	agaaaagaaa	ggatgcaagg	agtatgaaga	ggttccgaat	ctaaatattt	120
taatttataa	aaatcaattt	cgaattgaaa	ttcaactcct	actcgttttg	aaaatgccaa	180
tccttttaagt	aaacttctgg	atcgcccatt	tcttccagaa	attccttcaa	agtagtggtt	240
ttgtactgat	ttcctccgca	aagaatagga	actttcgaat	ctcctggagc	gaaacgggat	300
tttsataaca	aaaaactatc	cagacaaacc	ataggacttt	ttcaaatttt	ccttatttgg	360
ctgtccattt	ggaagcacc	aatctttaac	gctgtccagc	cagaagtgct	ccactcgcca	420
aggataaaag	gctcattttt	gaagccgaat	tttactaaaa	tctctagcca	tggagtcgat	480
ggatcagaaa	ttcgaggaat	tttagatttc	atcttgaaat	ttgcaatgga	aaaaataatt	540
attcaaagaa	aatcacagaa	aatgcaacaa	aaaaaacaaa	aaaagaacaa	aaaacaagtc	600
gaaaagtgcg	cccgggtcgt	ttgctgacgc	atctcttcaa	acgagacgcg	ctgctggcgc	660
acttctcgtg	ccctgtgcgt	gcatttccgc	aacaaaattc	aacacttggt	ttgaaacgca	720
ccgccctgtt	tcttttttca	attttgataa	gaaaatcagc	attgtttcag	gatgattaac	780

attccaactg	cgattctgtg	ccgcttgggc	gccagatcgt	cgatttcccg	ctcctttgga	840
acatcgatcg	tcaccaaggt	ggggattttt	tgaatttttc	cgtgaaaatt	gttgattttt	900
tgtgtacgca	tgaaggagaa	atgtataaca	gacacattct	tttcaattaa	ttatttataa	960
tattcacagt	ccgaggcaaa	gacgccaatc	cagaagtctg	gatgggaata	cctgttgaag	1020
cagcgctcca	agaatcgccc	aatcgctcca	catctcaccg	tctaccagcc	acaattgacc	1080
tgatgctct	ccggattcca	tagaatcagc	ggttgtgtaa	tggccggaac	ccttctcgtc	1140
ggaggaaatcg	gattcgcagt	tttgccgttc	gatttcacccg	cctttgtgga	tttcatccgt	1200
agctggaact	taccatgcgc	ggtgaccgct	gtcttcaagt	acatcattgc	tttccccatc	1260
attttccata	ctcttaacgg	aattcgcttc	ttaggattcg	atttggctaa	gggagtcaat	1320
aatgttggac	aggtaggagt	tgaatttatt	aatttaattg	ttttaaaaata	aaaattaatt	1380
ttcagatcta	caaatacgga	tatctcgtat	ctggactttc	ggctattctt	gctctcgcca	1440
ttgtcttcaa	ctcttgccag	aacaagagca	acaagactgc	ctaggcacag	atgctccgcc	1500
ttcttttttc	ttactccgcc	ccagccctcg	acaattctcg	tcaattttact	tttaccgttg	1560
atttcttcga	ttttctctct	tttccgtaga	tttacctctc	ctcttcggtt	ttttttctct	1620
gtctagaatg	tatattatga	ttatgaaaac	gaataaaaaat	tttagatgac	acgctgcacg	1680
gcggaacaact	cgctgacgaa	tccggcggtat	cggcgacgaa	cgatggcgac	tggcgagatg	1740
aaggagtttc	tggggataaa	aggcacagag	cccaccgatt	ttggaatcaa	tagtgatgct	1800
caggacttgc	catcaccgag	taggcaggct	tcgacgcgaa	gaatgtccat	cggagagtca	1860
attgatggaa	aaatcaatga	ttgggaagag	ccaaggcttg	atatcgaggg	atttgtggta	1920
attttttaat	ttttttttgt	aaataaaaat	tcctgctgct	tccaggtcga	ctatttcacg	1980
caccgaatcc	ggcaaaacgg	aatggaatgg	tttgagcac	cgggattgcc	gtgtggagtg	2040
caaccggagc	acgaaatgat	gcgagttatg	ggaacgatat	tcgagaagaa	gcacgcggaa	2100
aattttgaga	ccttctgtga	gcagctgctc	gcagtgccca	gaatctcatt	ttcactgtat	2160
caggatgtgg	ttcggacggt	tggaaatgca	cagacagatc	aatgtccaat	gtcttatgga	2220
cgtttggtaa	gggagaaaaat	actgaaaaaa	agtttgcaaa	aattcgaaaa	ttcgcagaa	2280
aggtggcaga	aaaaacattt	gcaaaaaattg	tttgttttcc	ttcaggaaat	cagcaaaact	2340
tgggtcaaaa	tagcccaatt	atgtgtcttt	tttgaaagtt	ttccattaaa	aaaccacgaa	2400
ttttgatccc	ggattgtaat	ttttttgtt	gataaattag	cagaaaaactt	tacgaattcg	2460
attaaaaacg	ttattttcta	ttcgaatatt	tttaaagcat	attttccttg	atttgtattt	2520
gcgaaaaaga	tctgctgatt	tatcaaaaaat	cggtttttaa	atgtaaaaat	tgtggaaaaat	2580
acattaaaaat	togatttttg	aacttttttc	ttcgaaaaac	aggtttttct	gctgatttgc	2640
tgaacgaaaa	accccaaaaa	ttcaattttc	gaacattaaa	aaaccagaaa	atcgtttttt	2700
taagcttaat	tttccgccag	aaatgaacga	attaaattgc	aaattttcta	ttttcagata	2760
ggtctaactc	cgttcggcgg	tttcgtagct	gcaaaaaatga	tggaaatccgt	ggaactgcag	2820
ggacaagtgc	gaaacctctt	cgtttacaca	tcgctgttca	tcaaaaacgg	gatccgcaac	2880
aactggaagg	aacacaatcg	gagctgggta	aggagtattt	gcatagacat	tagaagtcaa	2940
tatccccctt	tccttagtac	ccttgacttc	ccgggggtgt	ggtaagccga	taattacagg	3000
gttcggtagc	ctcttggggg	gacagctgga	aacatattca	agtatattac	tgtttatgat	3060
aatgttattg	ttacgggaat	acaaaattcg	cagaatgcta	tttcacaaca	tatttgacgc	3120
gcaaaaatc	cagtagagaa	aactacagta	attctttaaa	tttttaaaat	ttttacaatt	3180
aaagaaaaata	accactaatc	aaaagaaaat	aatttcaaaa	atcgagcccg	taaatcgact	3240
acagtaggca	tttaaagaat	tactgtagtt	ttcgctacga	gatatttccg	cctcaaatat	3300
gttgtgaaat	acgcattcac	ggatttttgt	gttccccgga	atatgctcta	aagcattatt	3360
atgaaagagg	actacgaacg	agcagaagct	gaaaaagtgg	tcatgacact	cggaaaaaca	3420
cggtggtcga	tgattggcgc	tggagtaaca	gctggagcca	gacgccggaa	gcagaacaga	3480
gtgtgtgggc	ggatgatgtt	cagcttgaag	taacgtatct	ttggaatcgt	tggagtctgc	3540
ttatgtacaa	ctccttacat	ttgaatctca	tttttgetca	aatttgtgta	aataattaat	3600
actggaagaa	gtgggaaaagc	taggccacaa	attacggctc	ctgattctct	catcctttga	3660
tactgcaatt	ttttccgatt	gccttttttt	ttggccaaac	tctgtgtcga	tttacgattt	3720
acttttccgt	gttctgtaca	tttcgtcaaa	aaccttgaaa	cctacttccg	cgtaatatca	3780
gcctagcctc	ccgcttctct	tccacatttc	caaagtaccc	ccctaacttt	tctcgccgtg	3840
ttcactttta	ctgtctcttt	tccgtgtggc	tcttccaact	ccccccaaat	ataattcatc	3900
gtacgcgact	ttgtatttat	ttttttcaaa	ttgttttctc	tctacaacaa	caaaaaaac	4020
ggttctttta	ttcaaccctt	ttttcggaac	gaaactgcaa	ttttgataat	aggcgtgcgc	4080
aagagaatcc	ggttttcatt	ttcgccatca	cgtcatccaa	aaaagttag	taggaaaaata	4140
tcatttttta	atataatgat	tcatctttct	cgcctcttct	gtctcgagac	gacgggtcaat	4200
togatggcct	tgaatttttc	gaaaacaaaa	atgtttttgt	ttagtgtaaa	cgatcccccc	4260

gccttatcgc tgtttcacca tcagataggc tccgccattt gattcccttg aattttgtcg 4320
gtatataaaa caaaaaacgt tagtgacaga ttcaaaaaac aacaatgcgt gctttactat 4380
tcacctctgt tgttcttttg gctttggctt ttgttgaggc aaagaagcag actatcactg 4440
tcaagggtag aactatttgc aataagaaga gaattcaggm graggttacc tttgggagaa 4500
agatactcgt gagttttcag tcttgtttag cttgaaacgg cttaaaaagg actaaaaagg 4560
cctaaaaatt gaagttttcc acctgttttc aaaagaaagc cgaattgcac agctttacac 4620
gagattttctc aataatttgc atttgaaatt ttcataattca tccccaaacg ttcctttacac 4680
gaaattttgc gatttttgag cttaaaaatac gatacctggt ctcgacacga aacatttttg 4740
ttaaattcaa aaagatgtgc gcctttaaag agtgctgtag tttgaaactt ctgttgttgc 4800
ggacttttca tcgatttttc gtagcgtttt tttataagaa aaatgtattt atttattcaa 4860
aaatttaatt ttaccgaatc gcgaaaaaca aaatgaagaa caccgataaa aatatcgag 4920
caacaatagt ttgaaattac agtactcttt taaggngnnc acatttcccta tatttcacac 4980
aaactgtcgt tgcgnnnn ggggtatcgtc attttgatgc agaaatcaag aaaattgcat 5040
atatgtttcaa aaaaccacaa ttatggcgaa tttcaagcct gaaacgaaaa ttcaggaaat 5100
tctaaaaatt aaaaaaaaat cattcgaaat gtgaaatttg atattcaact tgaagtccat 5160
atggcacaatt tcgtctattc cgnnnnttcga nnattttggt ccacgtggcc gcgaaaagag 5220
aaagcacgan nactgatttc tggcaatttt ttcctgtacc gtgtcaatta tttgaaactc 5280
taataagctg gtatttttct gctattgaca actaactgaa tccataattt gcaattataa 5340
tattgacttt tgatgtgtgg cttagaaaaa aaaaaccaaa aacctcatct agcttttaggc 5400
tgccaatata ttcctaggac atataaaaaa cccttaaaat tctctgcaac acctacaagc 5460
tatcaaacgt actattagta ttcaattttc cagtcgaccc cgatgacaag ctgcctcaa 5520
tgcaatcgaa caaagaagga gagttctcac ttaccggatc cgacgacgag atcacctcaa 5580
tctctccata cctcataatc acccacaact gcaacgtgaa gaaggccgga tgcaagcgtg 5640
tttcagagta tttgattcca aaggagaaga tcggtggaac ctatgatatg acatacgtca 5700
ctcttgatat tctttccgct aaagacaagg agaagtgcata agaaaatgtt ttttttgttt 5760
ggtttgcttg tttggaaggg aaggactttc tatctctttt aattcaacaa taaactattg 5820
gaaaaccggt gaaattttta ccttgaactg taagaaaagt tgcgtgatta tgttgacaat 5880
tttgccaagt atatctttgt ggatatcaca ataaacgaag tcaaagcacg aaatattacg 5940
gaaacacaaa attaatgaga atgcgcaaca tatttgaccg caaaatatct cgtagcgaag 6000
ctacagtaat tcttcaaaag actactgtag cgctgtgtcg atttacgagc tcgatttttg 6060
aaatgaatca gactagaaga aaaggaggaa aatattgaac atcaattgaa catcaattca 6120
aaaagtcgaa cccttgacta cagtagtctt ctaaaagaatt actgtagtgt tgcgtacgag 6180
atattttgng ngtcaaatat gttgngcaat acgcatcctc agaattgtgt gttctcgtaa 6240
tgtcttgaaa attttccatt tcaacatcaa ataagcaaat ctaaaaatgt ggggtctgca 6300
gcgaccacta tgactgtgat cgtggcaaga ccactcaga aaactacgtg ttccttttaa 6360
caaatacatt ttaagtatt gtaggtataa aaattgttgg ctagcagtct aggctgcctt 6420
tttcagtcga caaacttcta atttaatcgg cgggtcttca aaaagtcgtt tctttgaaaa 6480
tataaagctt tatatattta tatatataaa attttgatta catgatataa aaagcgacta 6540
gtttgtataa aaattatcaa 6560

<210> 2
<211> 1315
<212> DNA
<213> Caenorrrhabditis elegans

<220>
<221> CDS
<222> (7)...(846)

<400> 2
tttgag atg aca cgc tgc acg gcg gac aac tcg ctg acg aat ccg gcg 48
Met Thr Arg Cys Thr Ala Asp Asn Ser Leu Thr Asn Pro Ala
1 5 10
tat cgg cga cga acg atg gcg act ggc gag atg aag gag ttt ctg ggg 96
Tyr Arg Arg Arg Thr Met Ala Thr Gly Glu Met Lys Glu Phe Leu Gly

15	20	25	30	
ata aaa ggc aca gag	ccc acc gat ttt	gga atc aat agt	gat gct cag	144
Ile Lys Gly Thr Glu	Pro Thr Asp Phe Gly	Ile Asn Ser Asp	Ala Gln	
	35	40	45	
gac ttg cca tca ccg	agt agg cag gct	tcg acg cga aga	atg tcc atc	192
Asp Leu Pro Ser Pro	Ser Arg Gln Ala	Ser Thr Arg Arg	Met Ser Ile	
	50	55	60	
gga gag tca att gat	gga aaa atc aat	gat tgg gaa gag	cca agg ctt	240
Gly Glu Ser Ile Asp	Gly Lys Ile Asn	Asp Trp Glu Glu	Pro Arg Leu	
	65	70	75	
gat atc gag gga ttt	gtg gtc gac tat	ttc acg cac cga	atc cgg caa	288
Asp Ile Glu Gly Phe	Val Val Asp Tyr	Phe Thr His Arg	Ile Arg Gln	
	80	85	90	
aac gga atg gaa tgg	ttt gga gca ccg	gga ttg ccg tgt	gga gtg caa	336
Asn Gly Met Glu Trp	Phe Gly Ala Pro	Gly Leu Pro Cys	Gly Val Gln	
	95	100	105	110
ccg gag cac gaa atg	atg cga gtt atg	gga acg ata ttc	gag aag aag	384
Pro Glu His Glu Met	Met Arg Val Met	Gly Thr Ile Phe	Glu Lys Lys	
	115	120	125	
cac gcg gaa aat ttt	gag acc ttc tgt	gag cag ctg ctc	gca gtg ccc	432
His Ala Glu Asn Phe	Glu Thr Phe Cys	Glu Gln Leu Leu	Ala Val Pro	
	130	135	140	
aga atc tca ttt tca	ctg tat cag gat	gtg gtt ccg acg	gtt gga aat	480
Arg Ile Ser Phe Ser	Leu Tyr Gln Asp	Val Val Arg Thr	Val Gly Asn	
	145	150	155	
gca cag aca gat caa	tgt cca atg tct	tat gga cgt ttg	ata ggt cta	528
Ala Gln Thr Asp Gln	Cys Pro Met Ser	Tyr Gly Arg Leu	Ile Gly Leu	
	160	165	170	
atc tcg ttc ggc ggt	ttc gta gct gca	aaa atg atg gaa	tcc gtg gaa	576
Ile Ser Phe Gly Gly	Phe Val Ala Ala	Lys Met Met Glu	Ser Val Glu	
	175	180	185	190
ctg cag gga caa gtg	cga aac ctc ttc	gtt tac aca tcg	ctg ttc atc	624
Leu Gln Gly Gln Val	Arg Asn Leu Phe	Val Tyr Thr Ser	Leu Phe Ile	
	195	200	205	
aaa acg cgg atc cgc	aac aac tgg aag	gaa cac aat cgg	agc tgg gac	672
Lys Thr Arg Ile Arg	Asn Asn Trp Lys	Glu His Asn Arg	Ser Trp Asp	
	210	215	220	
gac ttc atg aca ctc	gga aaa caa atg	aaa gag gac tac	gaa cga gca	720
Asp Phe Met Thr Leu	Gly Lys Gln Met	Lys Glu Asp Tyr	Glu Arg Ala	
	225	230	235	
gaa gct gaa aaa gtg	gga cgc cgg aag	cag aac aga cgg	tgg tcg atg	768
Glu Ala Glu Lys Val	Gly Arg Arg Lys	Gln Asn Arg Arg	Trp Ser Met	
	240	245	250	

att ggc gct gga gta aca gct gga gcc att gga atc gtt gga gtc gtc 816
 Ile Gly Ala Gly Val Thr Ala Gly Ala Ile Gly Ile Val Gly Val Val
 255 260 265 270

gtg tgt ggg cgg atg atg ttc agc ttg aag taacgtattc aatttgtgta 866
 Val Cys Gly Arg Met Met Phe Ser Leu Lys
 275 280

aataattaat ttatgtacaa ctccttacat ttgaatctca ttttkgctca ctgattctct 926
 catcctttga actggaagaa gtgggaaagc taggccacaa attacggctc tctgtgtcga 986
 tttacgattt tactgcaatt ttttccgatt gccttttttt ttggccaaac cctacttccg 1046
 cgtaatatca acttttccgt gttctgtaca tttcgtcaaa aaccctgaaa ccctaacttt 1106
 tctcgccgtg gcctagcctc ccgcttctct tccacatttc caaagtaccc ctgtatctca 1166
 ataattcatc ttcactttaa ctgtctcttt tctgtgtggc tcttccaact ccccccaaat 1226
 tcctgtacgc gtacgcgact ttgtatttat ttttttcaaa ttgttttctc tctacaacaa 1286
 caaaaaaaaaa ggttcaaaaa aaaaaaaaaa 1315

<210> 3

<211> 280

<212> PRT

<213> Caenorhabditis elegans

<400> 3

Met Thr Arg Cys Thr Ala Asp Asn Ser Leu Thr Asn Pro Ala Tyr Arg
 1 5 10 15
 Arg Arg Thr Met Ala Thr Gly Glu Met Lys Glu Phe Leu Gly Ile Lys
 20 25 30
 Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln Asp Leu
 35 40 45
 Pro Ser Pro Ser Arg Gln Ala Ser Thr Arg Arg Met Ser Ile Gly Glu
 50 55 60
 Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu Asp Ile
 65 70 75 80
 Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln Asn Gly
 85 90 95
 Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln Pro Glu
 100 105 110
 His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys His Ala
 115 120 125
 Glu Asn Phe Glu Thr Phe Cys Glu Gln Leu Leu Ala Val Pro Arg Ile
 130 135 140
 Ser Phe Ser Leu Tyr Gln Asp Val Val Arg Thr Val Gly Asn Ala Gln
 145 150 155 160
 Thr Asp Gln Cys Pro Met Ser Tyr Gly Arg Leu Ile Gly Leu Ile Ser
 165 170 175
 Phe Gly Gly Phe Val Ala Ala Lys Met Met Glu Ser Val Glu Leu Gln
 180 185 190
 Gly Gln Val Arg Asn Leu Phe Val Tyr Thr Ser Leu Phe Ile Lys Thr
 195 200 205
 Arg Ile Arg Asn Asn Trp Lys Glu His Asn Arg Ser Trp Asp Asp Phe
 210 215 220
 Met Thr Leu Gly Lys Gln Met Lys Glu Asp Tyr Glu Arg Ala Glu Ala
 225 230 235 240
 Glu Lys Val Gly Arg Lys Gln Asn Arg Arg Trp Ser Met Ile Gly
 245 250 255
 Ala Gly Val Thr Ala Gly Ala Ile Gly Ile Val Gly Val Val Val Cys
 260 265 270
 Gly Arg Met Met Phe Ser Leu Lys

<210> 4
 <211> 1315
 <212> DNA
 <213> Caenorhabditis elegans

<220>
 <221> CDS
 <222> (7)...(846)

<400> 4
 tttgag atg aca cgc tgc acg gcg gac aac tcg ctg acg aat ccg gcg 48
 Met Thr Arg Cys Thr Ala Asp Asn Ser Leu Thr Asn Pro Ala
 1 5 10

tat cgg cga cga acg atg gcg act ggc gag atg aag gag ttt ctg ggg 96
 Tyr Arg Arg Arg Thr Met Ala Thr Gly Glu Met Lys Glu Phe Leu Gly
 15 20 25 30

ata aaa ggc aca gag ccc acc gat ttt gga atc aat agt gat gct cag 144
 Ile Lys Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln
 35 40 45

gac ttg cca tca ccg agt agg cag gct tcg acg cga aga atg tcc atc 192
 Asp Leu Pro Ser Pro Ser Arg Gln Ala Ser Thr Arg Arg Met Ser Ile
 50 55 60

gga gag tca att gat gga aaa atc aat gat tgg gaa gag cca agg ctt 240
 Gly Glu Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu
 65 70 75

gat atc gag gga ttt gtg gtc gac tat ttc acg cac cga atc cgg caa 288
 Asp Ile Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln
 80 85 90

aac gga atg gaa tgg ttt gga gca ccg gga ttg ccg tgt gga gtg caa 336
 Asn Gly Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln
 95 100 105 110

ccg gag cac gaa atg atg cga gtt atg gga acg ata ttc gag aag aag 384
 Pro Glu His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys
 115 120 125

cac gcg gaa aat ttt gag acc ttc tgt gag cag ctg ctc gca gtg ccc 432
 His Ala Glu Asn Phe Glu Thr Phe Cys Glu Gln Leu Leu Ala Val Pro
 130 135 140

aga atc tca ttt tca ctg aat cag gat gtg gtt ccg acg gtt gga aat 480
 Arg Ile Ser Phe Ser Leu Asn Gln Asp Val Val Arg Thr Val Gly Asn
 145 150 155

gca cag aca gat caa tgt cca atg tct tat gga cgt ttg ata ggt cta 528
 Ala Gln Thr Asp Gln Cys Pro Met Ser Tyr Gly Arg Leu Ile Gly Leu
 160 165 170

atc tcg ttc ggc ggt ttc gta gct gca aaa atg atg gaa tcc gtg gaa 576

Ile Ser Phe Gly Gly Phe Val Ala Ala Lys Met Met Glu Ser Val Glu
 175 180 185 190
 ctg cag gga caa gtg cga aac ctc ttc gtt tac aca tcg ctg ttc atc 624
 Leu Gln Gly Gln Val Arg Asn Leu Phe Val Tyr Thr Ser Leu Phe Ile
 195 200 205
 aaa acg cgg atc cgc aac aac tgg aag gaa cac aat cgg agc tgg gac 672
 Lys Thr Arg Ile Arg Asn Asn Trp Lys Glu His Asn Arg Ser Trp Asp
 210 215 220
 gac ttc atg aca ctc gga aaa caa atg aaa gag gac tac gaa cga gca 720
 Asp Phe Met Thr Leu Gly Lys Gln Met Lys Glu Asp Tyr Glu Arg Ala
 225 230 235
 gaa gct gaa aaa gtg gga cgc cgg aag cag aac aga cgg tgg tcg atg 768
 Glu Ala Glu Lys Val Gly Arg Lys Gln Asn Arg Arg Trp Ser Met
 240 245 250
 att ggc gct gga gta aca gct gga gcc att gga atc gtt gga gtc gtc 816
 Ile Gly Ala Gly Val Thr Ala Gly Ala Ile Gly Ile Val Gly Val Val
 255 260 265 270
 gtg tgt ggg cgg atg atg ttc agc ttg aag taacgtattc aatttgtgta 866
 Val Cys Gly Arg Met Met Phe Ser Leu Lys
 275 280
 aataattaat ttatgtacaa ctccctacat ttgaatctca ttttkgctca ctgattctct 926
 catcctttga actggaagaa gtgggaaagc taggccacaa attacggctc tctgtgtcga 986
 tttacgattt tactgcaatt ttttccgatt gccttttttt ttggccaaac cctacttcg 1046
 cgtaatatca acttttccgt gttctgtaca tttcgtcaaa aaccctgaaa ccctaacttt 1106
 tctcgccgtg gcttagcctc ccgcttctct tccacatttc caaagtaccc ctgtatctca 1166
 ataattcatc ttcactttaa ctgtctcttt tctgtgtggc tcttccaact ccccccaaat 1226
 tcctgtacgc gtacgcgact ttgtatttat ttttttcaaa ttgttttctc tctacaacaa 1286
 caaaaaaac ggttcaaaaa aaaaaaaaaa 1315
 <210> 5
 <211> 1315
 <212> DNA
 <213> Caenorhabditis elegans
 <220>
 <221> CDS
 <222> (7)...(846)
 <400> 5
 tttgag atg aca cgc tgc acg gcg gac aac tcg ctg acg aat ccg gcg 48
 Met Thr Arg Cys Thr Ala Asp Asn Ser Leu Thr Asn Pro Ala
 1 5 10
 tat cgg cga cga acg atg gcg act ggc gag atg aag gag ttt ctg ggg 96
 Tyr Arg Arg Arg Thr Met Ala Thr Gly Glu Met Lys Glu Phe Leu Gly
 15 20 25 30
 ata aaa ggc aca gag ccc acc gat ttt gga atc aat agt gat gct cag 144
 Ile Lys Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln
 35 40 45

gac ttg cca tca ccg agt agg cag gct tcg acg cga aga atg tcc atc 192
 Asp Leu Pro Ser Pro Ser Arg Gln Ala Ser Thr Arg Arg Met Ser Ile
 50 55 60

gga gag tca att gat gga aaa atc aat gat tgg gaa gag cca agg ctt 240
 Gly Glu Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu
 65 70 75

gat atc gag gga ttt gtg gtc gac tat ttc acg cac cga atc cgg caa 288
 Asp Ile Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln
 80 85 90

aac gga atg gaa tgg ttt gga gca ccg gga ttg ccg tgt gga gtg caa 336
 Asn Gly Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln
 95 100 105 110

ccg gag cac gaa atg atg cga gtt atg gga acg ata ttc gag aag aag 384
 Pro Glu His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys
 115 120 125

cac gcg gaa aat ttt gag acc ttc tgt gag cag ctg ctc gca gtg ccc 432
 His Ala Glu Asn Phe Glu Thr Phe Cys Glu Gln Leu Leu Ala Val Pro
 130 135 140

aga atc tca ttt tca ctg tat cag gat gtg gtt cgg acg gtt gga aat 480
 Arg Ile Ser Phe Ser Leu Tyr Gln Asp Val Val Arg Thr Val Gly Asn
 145 150 155

gca tag aca gat caa tgt cca atg tct tat gga cgt ttg ata ggt cta 528
 Ala * Thr Asp Gln Cys Pro Met Ser Tyr Gly Arg Leu Ile Gly Leu
 160 165 170

atc tcg ttc ggc ggt ttc gta gct gca aaa atg atg gaa tcc gtg gaa 576
 Ile Ser Phe Gly Gly Phe Val Ala Ala Lys Met Met Glu Ser Val Glu
 175 180 185

ctg cag gga caa gtg cga aac ctc ttc gtt tac aca tcg ctg ttc atc 624
 Leu Gln Gly Gln Val Arg Asn Leu Phe Val Tyr Thr Ser Leu Phe Ile
 190 195 200 205

aaa acg cgg atc cgc aac aac tgg aag gaa cac aat cgg agc tgg gac 672
 Lys Thr Arg Ile Arg Asn Asn Trp Lys Glu His Asn Arg Ser Trp Asp
 210 215 220

gac ttc atg aca ctc gga aaa caa atg aaa gag gac tac gaa cga gca 720
 Asp Phe Met Thr Leu Gly Lys Gln Met Lys Glu Asp Tyr Glu Arg Ala
 225 230 235

gaa gct gaa aaa gtg gga cgc cgg aag cag aac aga cgg tgg tcg atg 768
 Glu Ala Glu Lys Val Gly Arg Arg Lys Gln Asn Arg Arg Trp Ser Met
 240 245 250

att ggc gct gga gta aca gct gga gcc att gga atc gtt gga gtc gtc 816
 Ile Gly Ala Gly Val Thr Ala Gly Ala Ile Gly Ile Val Gly Val Val
 255 260 265

gtg tgt ggg cgg atg atg ttc agc ttg aag taacgtattc aatttgtgta 866
 Val Cys Gly Arg Met Met Phe Ser Leu Lys

aataattaat ttatgtacaa ctctttacat ttgaatctca ttttkgctca ctgattctct 926
catcctttga actggaagaa gtgggaaagc taggccacaa attacggctc tctgtgtcga 986
tttacgattt tactgcaatt ttttccgatt gccttttttt ttggccaaac cctacttccg 1046
cgtaatatca acttttccgt gttctgtaca ttctgtcaaa aaccctgaaa ccctaacttt 1106
tctcgccgtg gcctagcctc ccgcttctct tccacatttc caaagtaccc ctgtatctca 1166
ataattcatc ttcaatttaa ctgtctcttt tcgtgtggcc tcttccaact ccccccacaa 1226
tcctgtacgc gtacgcgact ttgtatttat ttttttcaaa ttgttttctc tctacaacaa 1286
caaaaaaac gggttcaaaa aaaaaaaaa 1315

<210> 6

<211> 1315

<212> DNA

<213> Caenorhabditis elegans

<220>

<221> CDS

<222> (7)...(846)

<400> 6

tttgag atg aca cgc tgc acg gcg gac aac tcg ctg acg aat ccg gcg 48
Met Thr Arg Cys Thr Ala Asp Asn Ser Leu Thr Asn Pro Ala
1 5 10
tat cgg cga cga acg atg gcg act ggc gag atg aag gag ttt ctg ggg 96
Tyr Arg Arg Arg Thr Met Ala Thr Gly Glu Met Lys Glu Phe Leu Gly
15 20 25 30
ata aaa ggc aca gag ccc acc gat ttt gga atc aat agt gat gct cag 144
Ile Lys Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln
35 40 45
gac ttg cca tca ccg agt agg cag gct tcg acg cga aga atg tcc atc 192
Asp Leu Pro Ser Pro Ser Arg Gln Ala Ser Thr Arg Arg Met Ser Ile
50 55 60
gga gag tca att gat gga aaa atc aat gat tgg gaa gag cca agg ctt 240
Gly Glu Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu
65 70 75
gat atc gag gga ttt gtg gtc gac tat ttc acg cac cga atc cgg caa 288
Asp Ile Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln
80 85 90
aac gga atg gaa tgg ttt gga gca ccg gga ttg ccg tgt gga gtg caa 336
Asn Gly Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln
95 100 105 110
ccg gag cac gaa atg atg cga gtt atg gga acg ata ttc gag aag aag 384
Pro Glu His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys
115 120 125
cac gcg gaa aat ttt gag acc ttc tgt gag cag ctg ctc gca gtg ccc 432
His Ala Glu Asn Phe Glu Thr Phe Cys Glu Gln Leu Leu Ala Val Pro
130 135 140
aga atc tca ttt tca ctg tat cag gat gtg gtt ccg acg gtt gga aat 480

Arg Ile Ser Phe Ser Leu Tyr Gln Asp Val Val Arg Thr Val Gly Asn
 145 150 155
 gca cag aca gat caa tgt cca atg tct tat gaa cgt ttg ata ggt cta 528
 Ala Gln Thr Asp Gln Cys Pro Met Ser Tyr Glu Arg Leu Ile Gly Leu
 160 165 170
 atc tcg ttc ggc ggt ttc gta gct gca aaa atg atg gaa tcc gtg gaa 576
 Ile Ser Phe Gly Gly Phe Val Ala Ala Lys Met Met Glu Ser Val Glu
 175 180 185 190
 ctg cag gga caa gtg cga aac ctc ttc gtt tac aca tcg ctg ttc atc 624
 Leu Gln Gly Gln Val Arg Asn Leu Phe Val Tyr Thr Ser Leu Phe Ile
 195 200 205
 aaa acg cgg atc cgc aac aac tgg aag gaa cac aat cgg agc tgg gac 672
 Lys Thr Arg Ile Arg Asn Asn Trp Lys Glu His Asn Arg Ser Trp Asp
 210 215 220
 gac ttc atg aca ctc gga aaa caa atg aaa gag gac tac gaa cga gca 720
 Asp Phe Met Thr Leu Gly Lys Gln Met Lys Glu Asp Tyr Glu Arg Ala
 225 230 235
 gaa gct gaa aaa gtg gga cgc cgg aag cag aac aga cgg tgg tcg atg 768
 Glu Ala Glu Lys Val Gly Arg Arg Lys Gln Asn Arg Arg Trp Ser Met
 240 245 250
 att ggc gct gga gta aca gct gga gcc att gga atc gtt gga gtc gtc 816
 Ile Gly Ala Gly Val Thr Ala Gly Ala Ile Gly Ile Val Gly Val Val
 255 260 265 270
 gtg tgt ggg cgg atg atg ttc agc ttg aag taacgtattc aatttggtga 866
 Val Cys Gly Arg Met Met Phe Ser Leu Lys
 275 280
 aataattaat ttatgtacaa ctccctacat ttgaatctca ttttkgctca ctgattctct 926
 catcctttga actggaagaa gtgggaaagc taggccacaa attacggctc tctgtgtcga 986
 tttacgattt tactgcaatt ttttccgatt gccttttttt ttggccaaac cctacttccg 1046
 cgtaatatca acttttccgt gttctgtaca tttcgtcaaa aaccctgaaa ccctaacttt 1106
 tctcgccgtg gcctagcctc ccgcttctct tccacatttc caaagtaccc ctgtatctca 1166
 ataattcatc ttcactttaa ctgtctcttt tctgtgtggc tcttccaact cccccaaat 1226
 tctgtacgc gtacgcgact ttgtatttat ttttttcaaa ttgttttctc tctacaacaa 1286
 caaaaaaac gggtcaaaaa aaaaaaaaaa 1315
 <210> 7
 <211> 5086
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1459) ... (2178)
 <400> 7
 ggcgccgccc ctccgcgcgc cctgcccgcg cgcccgcgcg gctcccgcgc gccgctctcc 60
 gtggcccccgc cgcgctgccc ccgcccgcgc tgccagcgaa ggtgccgggg ctccggggccc 120
 tccctgcccgc cggccgctcag cgctcggagc gaactgcgcg acgggaggtc cgggagggcga 180
 ccgtagtcgc gccgcgcgcg aggaccagga ggaggagaaa ggggtgcgcg cccggaggcg 240

ggggtgcgccg gtgggggtgca gcggaagagg ggggtccaggg gggagaaactt cgtagcagtc 300
 atcctttttta ggaaaagagg gaaaaaataa aacctcccc caccacctcc ttctccccac 360
 ccctgcgcgc accacacaca gcgcgggctt ctacgcgtcg gcaccggcgg gccaggcgcg 420
 tcctgccttc atttatccag cagcttttcg gaaaatgcat ttgctgttcg gagtttaatc 480
 agaagacgat tcctgcctcc gtccccggct ccttcacgt cccatctccc ctgtctctct 540
 cctggggagg cgtgaagcgg tcccgatgat agagattcat gcctgtgtcc gcgcgtgtgt 600
 gcgcgcgtat aaattgccga gaaggggaaa acatcacagg acttctgcga ataccggact 660
 gaaaattgta attcatctgc cgccgcgcgt gccaaaaaaa aactcgagct cttgagatct 720
 ccggttggga ttctgcgga ttgacatttc tgtgaagcag aagtctggga atcgatctgg 780
 aaatcctcct aatttttact cctctcccc cgaactcctg attcattggg aagtttcaaa 840
 tcagctataa ctggagagtg ctgaagattg atgggatcgt tgccttatgc atttgttttg 900
 gttttacaaa aaggaaactt gacagaggat catgctgtac ttaaaaaata caagtaagtc 960
 tcgcacagga aattgggtta atgtaacttt caatggaaac ctttgagatt ttttacttaa 1020
 agtgcatctg agtaaattta atttccaggc agcttaatac attgttttta gccgtgttac 1080
 ttgtagtggt tatgccctgc tttcactcag tgtgtacagg gaaacgcacc tgatttttta 1140
 cttattagtt tgttttttct ttaacctttc agcatcacag aggaagtaga ctgatattaa 1200
 caatacttac taataataac gtgcctcatg aaataaagat ccgaaaggaa ttggaataaa 1260
 aatttctgc gtctcatgcc aagagggaaa caccagaatc aagtgttccg cgtgattgaa 1320
 gacacccctc cgtccaagaa tgcaaagcac atccaataaa atagctggat tataactcct 1380
 cttctttctc tgggggcccgt ggggtgggag ctggggcgag aggtgccgtt ggcccccggt 1440
 gcttttctc tgggaagg atg gcg cac gct ggg aga acg ggg tac gac aac 1491
 Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn
 1 5 10

cgg gag ata gtg atg aag tac atc cat tat aag ctg tcg cag agg ggc 1539
 Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly
 15 20 25

tac gag tgg gat gcg gga gat gtg ggc gcc gcg ccc ccg ggg gcc gcc 1587
 Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala
 30 35 40

ccc gca ccg ggc atc ttc tcc tcc cag ccc ggg cac acg ccc cat cca 1635
 Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro His Pro
 45 50 55

gcc gca tcc cgc gac ccg gtc gcc agg acc tcg ccg ctg cag acc ccg 1683
 Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro
 60 65 70 75

gct gcc ccc ggc gcc gcc gcg ggg cct gcg ctc agc ccg gtg cca cct 1731
 Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro
 80 85 90

gtg gtc cac ctg gcc ctc cgc caa gcc ggc gac gac ttc tcc cgc cgc 1779
 Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg
 95 100 105

tac cgc ggc gac ttc gcc gag atg tcc agc cag ctg cac ctg acg ccc 1827
 Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro
 110 115 120

ttc acc gcg cgg gga cgc ttt gcc acg gtg gtg gag gag ctc ttc agg 1875
 Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg
 125 130 135

gac ggg gtg aac tgg ggg agg att gtg gcc ttc ttt gag ttc ggt ggg 1923
 Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly

140

145

150

155

gtc atg tgt gtg gag agc gtc aac cgg gag atg tgc ccc ctg gtg gac 1971
 Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp 170
 160

aac atc gcc ctg tgg atg act gag tac ctg aac cgg cac ctg cac acc 2019
 Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr 185
 175 180

tgg atc cag gat aac gga ggc tgg gat gcc ttt gtg gaa ctg tac ggc 2067
 Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly 200
 190 195

ccc agc atg cgg cct ctg ttt gat ttc tcc tgg ctg tct ctg aag act 2115
 Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr 215
 205 210

ctg ctc agt ttg gcc ctg gtg gga gct tgc atc acc ctg ggt gcc tat 2163
 Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr 235
 220 225 230

ctg agc cac aag tga agtcaacatg cctgccccaa acaaatatgc aaaaggttca 2218
 Leu Ser His Lys *

ctaaagcagt agaaataata tgcattgtca gtgatgtacc atgaaacaaa gctgcaggct 2278
 gtttaagaaa aaataacaca catataaaca tcacacacac agacagacac acacacacac 2338
 aacaattaac agtccttcagg caaaacgtcg aatcagctat ttactgcaa agggaaatat 2398
 catttatttt ttacattatt aagaaaaaag atttatttat ttaagacagt cccatcaaaa 2458
 ctccgtcttt ggaaatccga ccactaattg ccaaacaccg cttcgtgtgg ctccacctgg 2518
 atgttctgtg cctgtaaaca tagattcgct ttccatgttg ttggccggat caccatctga 2578
 agagcagacg gatggaaaaa ggacctgac ttccatgttg ctggccttct ggctgctgga 2638
 ggctggggag aaggtgttca ttcacttgca tttctttgcc ctgggggctg gatattaaca 2698
 gagggagggt tccgtgggg ggaagtccat gcctccctgg cctgaagaag agactctttg 2758
 catatgactc acatgatgca tacctgggtg gaggaaaaga gttgggaact tcagatggac 2818
 ctagtaccce ctgagatttc cacgccgaag gacagcgatg ggaaaaatgc ccttaaatca 2878
 taggaaagta tttttttaag ctaccaattg tgccgagaaa agcatttttag caattttatac 2938
 aatatcatcc agtaccttaa accctgattg tgtatattca tatatttttg atacgcaccc 2998
 cccaactccc aatactggct ctgtctgagt aagaaacaga atcctctgga acttgaggaa 3058
 gtgaacattt cgggtgacttc cgatcaggaa ggctagagtt acccagagca tcaggccgcc 3118
 acaagtgcct gcttttagga gaccgaagtc cgcagaacct acctgtgtcc cagcttgagg 3178
 gcctggctct ggaactgagc cgggccctca ctggcctcct ccagggatga tcaacagggt 3238
 agtggtgtct ccgaatgtct ggaagctgat ggatggagct cagaattcca ctgtcaagaa 3298
 agagcagtag aggggtgtgg ctgggcctgt caccctgggg tatcactgta gagggaagga 3418
 tcacgtggag cataggagcc acgacccttc ttaagacatg ggctgggaac gtgaggagag 3478
 acagaggccc tgggccttcc tatcagaagg acatggcacg ttggctgtgt ggccttgccc 3538
 gcaatggcca cgccccattt tggctgtagc actttggaga gggtcacaaa tcctaaaaga 3598
 acctgtgagt ttaaagcaag gctttaaatg gaccctgtc tatggaatta catgtaaaac 3658
 agcattgaag tgagggtgtca tggattaatt tgaaaacctg acaaaaaaaa agttccagg 3718
 attatcttgt cactgtagtt tggttttatt gggcattaaa aaaaaatcaa tgggtgggaa 3778
 gtggaatatg ggggttatct gtacatcctg ttcagcaaat aaactaggaa attttttttt 3838
 ctataaagaa gtaacaaaag aagtgcacac gatggaataa ctctgtggca ttattgcatt 3898
 cttccagttt agaatcagcc ttgaaacatt tgtactctgt tcaatgttta atgctgtggt 3958
 atataccatt tatctgtatt aactttggaa catgcacctc agcgtttttt tgtttttaat 4018
 tgatatttcg aaagctgctt taaaaaata tgagcaaagg tgatcgtttt ctgtttgaga 4078
 tgtatttagt tatggcctat acactatttg tgagaagggt agataagccc tgagtctcag 4138
 tttttatctc ttgattcttc aaaagcattc

ctacctaaga aaaacctgga tgtcactggc cactgaggag ctttgtttca accaagtcac 4198
 gtgcatttcc acgtcaacag aattgtttat tgtgacagtt atatctgttg tccctttgac 4258
 cttgttttctt gaagggtttcc tcgtccctgg gcaattccgc atttaattca tgggtattcag 4318
 gattacatgc atgttttggtt aaacccatga gattcattca gttaaaaatc cagatggcga 4378
 atgaccagca gattcaaatc tatggtgggtt tgacctttag agagttgctt tacgtggcct 4438
 gtttcaacac agacccaccc agagccctcc tgccctcctt ccgcgggggc tttctcatgg 4498
 ctgtccttca ggggtcttcc gaaatgcagt ggtcggttacg ctccaccaag aaagcaggaa 4558
 acctgtggta tgaagccaga cctccccggc gggcctcagg gaacagaatg atcagacctt 4618
 tgaatgattc taatttttaa gcaaaatatt attttatgaa aggtttacat tgtcaaagt 4678
 atgaatatgg aatatccaat cctgtgctgc tatectgcca aaatcatttt aatggagtca 4738
 gtttgacgta tgctccacgt ggtaagatcc tccaagctgc tttagaagta acaatgaaga 4798
 acgtggacgt ttttaataa aagcctgttt tgtcttttgt tgtgtttcaa acgggattca 4858
 cagagtattt gaaaaatgta tatatattaa gaggtcacgg gggctaattg ctagctggct 4918
 gccttttgct gtgggggtttt gttacctggg ttttaataca gtaaagtgtc ccagcctcct 4978
 ggccccagaa ctgtacagta ttgtggctgc acttgctcta agagtagttg atgttgacatt 5038
 ttccttattg ttaaaaacat gttagaagca atgaatgtat ataaaagc 5086

<210> 8

<211> 239

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1 5 10 15
 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
 20 25 30
 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
 35 40 45
 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60
 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80
 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
 85 90 95
 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
 100 105 110
 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
 115 120 125
 Arg Phe Ala Thr Val Val Glu Leu Phe Arg Asp Gly Val Asn Trp
 130 135 140
 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
 145 150 155 160
 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175
 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190
 Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
 195 200 205
 Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
 210 215 220
 Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys
 225 230 235